

F. Molzie

1653

F#10

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/325,602A DATE: 12/05/2000  
TIME: 14:25:40

Input Set : A:\Onv06902.app  
Output Set: N:\CRF3\12052000\I325602A.raw

RECEIVED

DEC 15 2000

TECH CENTER 1500/2900

3 <110> APPLICANT: Galdes, Alphonse  
4 Mahanthappa, Nagesh  
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING DISORDERS INVOLVING  
7 EXCITOTOXICITY  
9 <130> FILE REFERENCE: BIV-069.02  
11 <140> CURRENT APPLICATION NUMBER: 09/325,602A  
12 <141> CURRENT FILING DATE: 1999-06-03  
14 <150> PRIOR APPLICATION NUMBER: 09/238,243  
15 <151> PRIOR FILING DATE: 1999-01-27  
17 <160> NUMBER OF SEQ ID NOS: 32  
19 <170> SOFTWARE: PatentIn Ver. 2.1  
21 <210> SEQ ID NO: 1  
22 <211> LENGTH: 1277  
23 <212> TYPE: DNA  
24 <213> ORGANISM: Gallus sp.  
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27 <221> NAME/KEY: CDS  
28 <222> LOCATION: (1)..(1275)  
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32 Met Val Glu Met Leu Leu Leu Thr Arg Ile Leu Leu Val Gly Phe Ile  
33 1 5 10 15  
35 tgc gct ctt tta gtc tcc tct ggg ctg act tgt gga cca ggc agg ggc 96  
36 Cys Ala Leu Leu Val Ser Ser Gly Leu Thr Cys Gly Pro Gly Arg Gly  
37 20 25 30  
39 att gga aaa agg agg cac ccc aaa aag ctg acc cgg tta gcc tat aag 144  
40 Ile Gly Lys Arg Arg His Pro Lys Lys Leu Thr Pro Leu Ala Tyr Lys  
41 35 40 45  
43 cag ttt att ccc aat gtg gca gag aag acc cta ggg gcc agt gga aga 192  
44 Gln Phe Ile Pro Asn Val Ala Glu Lys Thr Leu Gly Ala Ser Gly Arg  
45 50 55 60  
47 tat gaa ggg aag atc aca aga aac tcc gag aga ttt aaa gaa cta acc 240  
48 Tyr Glu Gly Lys Ile Thr Arg Asn Ser Glu Arg Phe Lys Glu Leu Thr  
49 65 70 75 80  
51 cca aat tac aac cct gac att att ttt aag gat gaa gag aac acg gga 288  
52 Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Thr Gly  
53 85 90 95  
55 gct gac aga ctg atg act cag cgc tgc aag gac aag ctg aat gcc ctg 336  
56 Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Lys Leu Asn Ala Leu  
57 100 105 110  
59 cgc atc tcg gtg atg aac cag tgg ccc ggg gtg aag ctg cgg gtg acc 384  
60 Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg Val Thr  
61 115 120 125  
63 gag ggc tgg gac gag gat ggc cat cac tcc gag gaa tcg ctg cac tac 432  
64 Glu Gly Trp Asp Glu Asp Gly His His Ser Glu Glu Ser Leu His Tyr  
65 130 135 140  
67 gag ggt cgc gcc gtg gac atc acc acg tcg gat cgg gac cgc agc aag 480

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68 Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg Ser Lys
69 145 150 155 160
71 tac gga atg ctg gcc cgc ctc gcc gtc gag gcc gcc ttc gac tgg gtc 528
72 Tyr Gly Met Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val
73 165 170 175
75 tac tac gag tcc aag gcg cac atc cac tgc tcc gtc aaa gca gaa aac 576
76 Tyr Tyr Glu Ser Lys Ala His Ile His Cys Ser Val Lys Ala Glu Asn
77 180 185 190
79 tca gtg gca gcg aaa tca gga gcc tgc ttc cct gcc tca gcc aca gtg 624
80 Ser Val Ala Ala Lys Ser Gly Gly Cys Phe Pro Gly Ser Ala Thr Val
81 195 200 205
83 cac ctg gag cat gga gcc acc aag ctg gtg aag gac ctg agc cct ggg 672
84 His Leu Glu His Gly Gly Phe Lys Leu Val Lys Asp Leu Ser Pro Gly
85 210 215 220
87 gac cgc gtg ctg gct gct gac gcg gac gcc cgg ctg ctc tac agt gac 720
88 Asp Arg Val Leu Ala Ala Asp Ala Asp Gly Arg Leu Leu Tyr Ser Asp
89 225 230 235 240
91 ttc ctc acc ttc ctc gac cgg atg gac agc tcc cga aag ctc ttc tac 768
92 Phe Leu Thr Phe Leu Asp Arg Met Asp Ser Ser Arg Lys Leu Phe Tyr
93 245 250 255
95 gtc atc gag acg cgg cag ccc cgg gcc cgg ctg cta ctg acg gcg gcc 816
96 Val Ile Glu Thr Arg Gln Pro Arg Ala Arg Leu Leu Leu Thr Ala Ala
97 260 265 270
99 cac ctg ctc ttt gtg gcc ccc cag cac aac cag tcy gag gcc aca ggg 864
100 His Leu Leu Phe Val Ala Pro Gln His Asn Gln Ser Glu Ala Thr Gly
101 275 280 285
103 tcc acc agt gcc cag gcg ctc ttc gcc agc aac gtg aag cct gcc caa 912
104 Ser Thr Ser Gly Gln Ala Leu Phe Ala Ser Asn Val Lys Pro Gly Gln
105 290 295 300
107 cgt gtc tat gtg ctg gcc gag gcc ggg cag cag ctg ctg ccg gcg tct 960
108 Arg Val Tyr Val Leu Gly Glu Gly Gly Gln Gln Leu Leu Pro Ala Ser
109 305 310 315 320
111 gtc cac agc gtc tca ttg cgg gag gag gcg tcc gga gcc tac gcc cca 1008
112 Val His Ser Val Ser Leu Arg Glu Gln Ala Ser Gly Ala Tyr Ala Pro
113 325 330 335
115 ctc acc gcc cag gcc acc atc ctc atc aac cgg gtg ttg gcc tcc tgc 1056
116 Leu Thr Ala Gln Gly Thr Ile Leu Ile Asn Arg Val Leu Ala Ser Cys
117 340 345 350
119 tac gcc gtc atc gag gag cac agt tgg gcc cat tgg gcc ttc gca cca 1104
120 Tyr Ala Val Ile Glu Glu His Ser Trp Ala His Trp Ala Phe Ala Pro
121 355 360 365
123 ttc cgc ttg gct cag ggg ctg ctg gcc gcc ctc tgc cca gat ggg gcc 1152
124 Phe Arg Leu Ala Gln Gly Leu Leu Ala Ala Leu Cys Pro Asp Gly Ala
125 370 375 380
127 atc cct act gcc gcc acc acc acc act gcc atc cat tgg tac tca cgg 1200
128 Ile Pro Thr Ala Ala Thr Thr Thr Thr Gly Ile His Trp Tyr Ser Arg
129 385 390 395 400
131 ctc ctc tac cgc atc gcc agc tgg gtg ctg gat ggt gac gcg ctg cat 1248
132 Leu Leu Tyr Arg Ile Gly Ser Trp Val Leu Asp Gly Asp Ala Leu His

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133                               405                               410                               415
135 ccg ctg ggc atg gtg gca ccg gcc agc tg                               1277
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137                               420                               425
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140 <211> LENGTH: 1190
141 <212> TYPE: DNA
142 <213> ORGANISM: Murine sp.
144 <220> FEATURE:
145 <221> NAME/KEY: CDS
146 <222> LOCATION: (1)..(1188)
148 <400> SEQUENCE: 2
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151 1 5 10 15
153 gca cta tct gcc caq agc tgc ggc ccg ggc cga gga ccg gtt ggc cgg 96
154 Ala Leu Ser Ala Gln Ser Cys Gly Pro Gly Arg Gly Pro Val Gly Arg
155 20 25 30
157 cgg cgt tat gtg cgc aag caa ctt gtg cct ctg cta tac aag cag ttt 144
158 Arg Arg Tyr Val Arg Lys Gln Leu Val Pro Leu Leu Tyr Lys Gln Phe
159 35 40 45
161 gtg ccc agt atg ccc gag cgg acc ctg ggc gcg agt ggg cca gcg gag 192
162 Val Pro Ser Met Pro Glu Arg Thr Leu Gly Ala Ser Gly Pro Ala Glu
163 50 55 60
165 ggg aag qta aca aag ggc tgc gag cgc ttc cgg gac ctc gta ccc aac 240
166 Gly Arg Val Thr Arg Gly Ser Glu Arg Phe Arg Asp Leu Val Pro Asn
167 65 70 75 80
169 tac aac ccc gac ata atc ttc aag gat gag gag aac agc ggc gca gac 288
170 Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn Ser Gly Ala Asp
171 85 90 95
173 cgc ctg atg aca gag cgt tgc aaa gag cgg gtg aac gct cta gcc atc 336
174 Arg Leu Met Thr Glu Arg Cys Lys Glu Arg Val Asn Ala Leu Ala Ile
175 100 105 110
177 gcg gtg atg aac atg tgg ccc gga gta cgc cta cgt gtg act gaa ggc 384
178 Ala Val Met Asn Met Trp Pro Gly Val Arg Leu Arg Val Thr Glu Gly
179 115 120 125
181 tgg gac gag gac gcc cac cac gca cag gat tca ctc cac tac gaa ggc 432
182 Trp Asp Glu Asp Gly His His Ala Gln Asp Ser Leu His Tyr Glu Gly
183 130 135 140
185 cgt gcc ttg gac atc acc acg tct gac cgt gac cgt aat aag tat ggt 480
186 Arg Ala Leu Asp Ile Thr Thr Ser Asp Arg Asp Arg Asn Lys Tyr Gly
187 145 150 155 160
189 ttg ttg gcg cgc cta gct ttg gaa gcc gga ttc gac tgg gtc tac tac 528
190 Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp Trp Val Tyr Tyr
191 165 170 175
193 gag tcc cgc aac cac atc cac gta tgc gtc aaa gct gat aac tca ctg 576
194 Glu Ser Arg Asn His Ile His Val Ser Val Lys Ala Asp Asn Ser Leu
195 180 185 190
197 gcg gtc cga gcc gga ggc tgc ttt ccg gga aat gcc acg gtg cgc ttg 624

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198 Ala Val Arg Ala Gly Gly Cys Phe Pro Gly Asn Ala Thr Val Arg Leu
199          195          200          205
201 cag aac ggc gaa cag aag ggg ctg agg gaa cta cat cgt ggt gac tgg 672
202 Arg Ser Gly Glu Arg Lys Gly Leu Arg Glu Leu His Arg Gly Asp Trp
203          210          215          220
205 gta ctg gcc gct gat gca gcg ggc cga gtg gta ccc acg cca gty ctg 720
206 Val Leu Ala Ala Asp Ala Ala Gly Arg Val Val Pro Thr Pro Val Leu
207 225          230          235          240
209 ctg ttc ctg gac cgg gat ctg cag cgc cgc gcc tgg ttc gty gct gty 768
210 Leu Phe Leu Asp Arg Asp Leu Gln Arg Arg Ala Ser Phe Val Ala Val
211          245          250          255
213 gag acc gag cag cct ccg cgc aaa ctg ttg ctg aca ccc tgg cat ctg 816
214 Glu Thr Glu Arg Pro Pro Arg Lys Leu Leu Leu Thr Pro Trp His Leu
215          260          265          270
217 gty ttc gct gct cgc ggg cca gcg cct gct cca ggt gac ttt gca ccg 864
218 Val Phe Ala Ala Arg Gly Pro Ala Pro Ala Pro Gly Asp Phe Ala Pro
219          275          280          285
221 gty ttc gcg cgc cgc tta cgt gct ggc gac tgg gty ctg gct ccc ggc 912
222 Val Phe Ala Arg Arg Leu Arg Ala Gly Asp Ser Val Leu Ala Pro Gly
223          290          295          300
225 ggg gac gcg ctg cag ccg gcg cgc gta gcc cgc gty gcg cgc gag gaa 960
226 Gly Asp Ala Leu Gln Pro Ala Arg Val Ala Arg Val Ala Arg Glu Glu
227 305          310          315          320
229 gcc gty q. gty ttc gca ccg ctg act gcg cac ggg acg ctg ctg gtc 1008
230 Ala Val Gly Val Phe Ala Pro Leu Thr Ala His Gly Thr Leu Leu Val
231          325          330          335
233 aac gac gtc ctg gcc tcc tgc tac gcg gtt cta gag agt cac cag tgg 1056
234 Asn Asp Val Leu Ala Ser Cys Tyr Ala Val Leu Glu Ser His Gln Trp
235          340          345          350
237 gcc cac cgc gcc ttc gcc cct ttg cgg ctg ctg cac gcg ctg ggg gct 1104
238 Ala His Arg Ala Phe Ala Pro Leu Arg Leu Leu His Ala Leu Gly Ala
239          355          360          365
241 ctg ctg cct ggg ggt gca gtc cag ccg act gcc atg cat tgg tac tct 1152
242 Leu Leu Pro Gly Gly Ala Val Gln Pro Thr Gly Met His Trp Tyr Ser
243          370          375          380
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247 385          390          395
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251 <211> LENGTH: 1281
252 <212> TYPE: DNA
253 <213> ORGANISM: Murine sp.
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256 <221> NAME/KEY: CDS
257 <222> LOCATION: (1)..(1233)
259 <400> SEQUENCE: 3
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262 1          5          10          15

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264 ctg ctg ctg ctt ctg gtg ccg gcg gcg ccg ggc tgc ggg ccg ggc ccg 96
265 Leu Leu Leu Leu Leu Val Pro Ala Ala Arg Gly Cys Gly Pro Gly Arg
266      20      25      30
268 gtg gtg ggc agc cgc ccg agc ccg cct cgc aag ctc gtg cct ctt gcc 144
269 Val Val Gly Ser Arg Arg Arg Pro Arg Lys Leu Val Pro Leu Ala
270      35      40      45
272 tac aag cag ttc agc ccc aac gtg ccg gag aag acc ctg ggc gcc aac 192
273 Tyr Lys Gln Phe Ser Pro Asn Val Pro Glu Lys Thr Leu Gly Ala Ser
274      50      55      60
276 ggg cgc tac gaa ggc aag atc gcg cgc agc tct gag cgc ttc aaa gag 240
277 Gly Arg Tyr Glu Gly Lys Ile Ala Arg Ser Ser Glu Arg Phe Lys Glu
278      65      70      75      80
280 ctc acc ccc aac tac aat ccc gac atc atc ttc aag gac gag gag aac 288
281 Leu Thr Pro Asn Tyr Asn Pro Asp Ile Ile Phe Lys Asp Glu Glu Asn
282      85      90      95
284 acg ggt gcc gac cgc ctc atg acc cag cgc tgc aag gac cgt ctg aac 336
285 Thr Gly Ala Asp Arg Leu Met Thr Gln Arg Cys Lys Asp Arg Leu Asn
286      100      105      110
288 tca ctg gcc atc tct gtc atg aac cag tgg cct ggt gtg aaa ctg ccg 384
289 Ser Leu Ala Ile Ser Val Met Asn Gln Trp Pro Gly Val Lys Leu Arg
290      115      120      125
292 gtg acc gaa ggc ccg gat gaa gat gcc cat cac tca gag gag tct tta 432
293 Val Thr Glu Gly Arg Asp Glu Asp Gly His His Ser Glu Glu Ser Leu
294      130      135      140
296 cac tat gag ggc cgc gcg gtg gat atc acc acc tca gac cgt gac cga 480
297 His Tyr Glu Gly Arg Ala Val Asp Ile Thr Thr Ser Asp Arg Asp Arg
298      145      150      155      160
300 aat aag tat gga ctg ctg gcg cgc tta gca gtg gag gcc ggc ttc gac 528
301 Asn Lys Tyr Gly Leu Leu Ala Arg Leu Ala Val Glu Ala Gly Phe Asp
302      165      170      175
304 tgg gtg tat tac gag tcc aag gcc cac gtg cat tgc tct gtc aag tct 576
305 Trp Val Tyr Tyr Glu Ser Lys Ala His Val His Cys Ser Val Lys Ser
306      180      185      190
308 gag cat tgc gcc gct gcc aag aca ggt ggc tgc ttt cct gcc gga gcc 624
309 Glu His Ser Ala Ala Ala Lys Thr Gly Gly Cys Phe Pro Ala Gly Ala
310      195      200      205
312 cag gtg cgc cta gag aac ggg gag cgt gtg gcc ctg tca gct gta aag 672
313 Gln Val Arg Leu Glu Asn Gly Glu Arg Val Ala Leu Ser Ala Val Lys
314      210      215      220
316 cca gga gac ccg gtg ctg gcc atg ggg gag gat ggg acc ccc acc ttc 720
317 Pro Gly Asp Arg Val Leu Ala Met Gly Glu Asp Gly Thr Pro Thr Phe
318      225      230      235      240
320 aqt gat gtg ctt att ttc ctg gac cgc gag cca aac ccg ctg aga gct 768
321 Ser Asp Val Leu Ile Phe Leu Asp Arg Glu Pro Asn Arg Leu Arg Ala
322      245      250      255
324 ttc cag gtc atc gag act cag gat cct ccg cgt ccg ctg gcg ctc acg 816
325 Phe Gln Val Ile Glu Thr Gln Asp Pro Pro Arg Arg Leu Ala Leu Thr
326      260      265      270
328 cct gcc cac ctg ctc ttc att gcg gac aat cat aca gaa cca gca gcc 864

```

**FYI:**

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/325,602A

DATE: 12/05/2000

TIME: 14:25:41

Input Set : A:\Onv06902.app

Output Set: N:\CRF3\12052000\I325602A.raw

L:733 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:734 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:1620 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:2247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2253 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
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L:2286 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
L:2525 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:2528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
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L:2555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22